



SEQUENCE LISTING

<110>Ulrich, Ricky
Jeddeloh, Jeffrey A.
Oyston, Petra

<120> Glanders/Melioidosis Vaccines

<130> 003/267/SAP

<140> 10/620,242

<141> 2003-07-15

<150> US 60/386,257

<151> 2002-07-15

<160> 44

<170> Apple Macintosh Microsoft Word 6.0

<210> 1

<211> 612

<212> DNA

<213> *B. mallei* ATCC 23344 AHS gene *bmaI1*

<400> 1

atgcgaactt	tcgtttcatgg	cgacggggcgc	ctgccgagcg	40
acttggcggc	tgatctgggc	ctttatcggc	acggagtttt	80
cgctcgagcag	ctcggctgga	aactgccgtc	ggcaagcgaa	120
gggttcgagc	gggatcagta	cgatcgcgac	gataccgtct	160
atgtgttcgc	ccgcgacgac	gacggggaaa	tctgcggctg	200
cgcccggctg	ctgccgacga	cccggccgta	tctgctgaag	240
gaactgttcc	cgacgctggg	cgcgcaagac	atgccgttgc	280
cgcaatccgc	cgccgtctgg	gaattgtcgc	gcttcgccgc	320
gaacgccgag	gatccggccg	ggggcggcaa	cccggcctgg	360
gcggtgcgcc	cgatgtctgc	cgccgtcgtc	gagtgcgccg	400
cgcggtcttg	cgcgaaagcaa	ctgatcggcg	tgacgtttct	440
gagcatggag	cgccgtgttc	gccggatcgg	cgtgcacgcg	480
caccgggcgg	ggcccgcgca	gcagatcgac	gggcgcgatg	520
tcgtcgcgtg	ctggatcgac	ctcgacgcgc	aaacgctcgc	560
cgcgctcgat	ctcgaccgcg	tgctgtgcgc	gccgcccgcc	600
gaagccgcct	ga			612

<210> 2

<211> 609

<212> DNA

<213> *B. mallei* ATCC 23344 AHS gene *bmaI3*

<400> 2

atgtcataca	tcatcgcggg	ccgattgaac	gaactgccgc	40
cgcacgtcca	gaccgatctc	ggcgcgtatc	gctacgacgt	80

```

gttcgtgcgc cggctcggct ggacgatcgc cggccactcg 120
ctcgacgaac atgcggagtg ggacgagttc gacgggccgt 160
cgacgattca tgtcgtcgcg ctcgacgacg cgcgcgagat 200
ctgcggctac gcacgcctgc tgccgacgac gggcccgtat 240
ctgctgcgcg acgtgtttgc gcatctgctc ggctcgtcgc 280
ccgcgccgca atcgcttgcg gtctgggaaa tgtcgcgctt 320
cgccgcgtcg cggcggcggc gaagcgcgac cgagcgcgag 360
ccgctcggca tggcgcttct tccgtcggtg ctcacggtgg 400
ccgcgtcgtc cggcgcgacg cgcgtggtcg gcgtgatgac 440
gccatcgatc gaacgcctgt accgccgctc gggcatcgcg 480
ctgcacgcgc tcggcaacgc gatgccgggc gcgggcggca 520
gctgttcgcg atgctcgatc gatctgccgc gcctcgcgtt 560
cgcgccgttg ggcctcaagc agtgcgcggc gtgcctggcg 600
atgcattga 609

```

<210> 3

<211> 720

<212> DNA

<213> *B. mallei* ATCC 23344 transcriptional regulator gene
bmaR1

<400> 3

```

atggaactgc gctggcaaga cgcttatctt caatttagcg 40
ccgcggagaa cgagcagcag ctcttccaac agatcgccgc 80
gtatacgaag cggctcggct tcgaatattg ctgctatggc 120
atacgcgtgc cgcttgccgat ctgaagccg gtcgtcgcga 160
ttttcgacac ctatccgaac ggctggatgg agcgtacca 200
ggaaatgaac tacctggagg tcgatccgac cgtacgcgag 240
ggcgcgctca gctcgaacat gatcgtctgg ccggaggcga 280
gcgcgagcga cgcgacgacg ctctggagcg acgcgcgcga 320
tcacgggctg gcggtcggcg tcgcgcagtc gagctgggcc 360
tcgcgcgggg tgttcggtct cctgacgata gcgcggcaca 400
cggaccgcct gacgtccgcc gagatcaacc atctgacgtt 440
gcaggcgaac tggctcgcga acatgtcgca ctcgctgatg 480
agccgttttc tcgtgccgaa gctcgcgccc gaatcgggcg 520
tggcgctcac gcaccgcgag cgggaggtgc tgtgctggac 560
gggagagggc aagaccgcgt gcgagatcgg gcagatcctc 600
agcatctccg agcgcacggt gaactttcac gtcaacaaca 640
tcctcgacaa gctcggcgcg acgaacaagg tgcaggccgt 680
cgtgaaggcg atcgcgatgg ggctcatcga cgcgccgtaa 720

```

<210> 4

<211> 609

<212> DNA

<213> *B. mallei* ATCC 23344 transcriptional regulator gene
bmaR3

<400> 4

```

atgtcataca tcatcgcggg ccgattgaac gaactgccgc 40
cgcacgtcca gaccgatctc ggccgcgtatc gctacgacgt 80
gttcgtgcgc cggctcggct ggacgatcgc cggccactcg 120
ctcgacgaac atgcggagtg ggacgagttc gacgggccgt 160
cgacgattca tgtcgtcgcg ctcgacgacg cgcgcgagat 200
ctgcggctac gcacgcctgc tgccgacgac gggcccgtat 240
ctgctgcgcg acgtgtttgc gcatctgctc ggctcgtcgc 280

```

```

ccgcgcgcga atcgccctgcc gtctgggaaa tgtcgcgctt 320
cgccgcgctcg cggcgggcggc gaagcgcgac cgaccgcgag 360
ccgctcggca tggcggttctt tccgtcgggtg ctcacgggtgg 400
ccgcgtcgct cggcgcgacg cgcgtgggtcg gcgtgatgac 440
gccatcgatc gaacgcctgt accgccgctc gggcatcgcg 480
ctgcatcgcc tcggcaacgc gatgccgggc gcgggcggca 520
gcctgtccgc atgctcgatc gatctgccgc gcctcgcgtt 560
cgcgccggtt ggctcaagc agtgcgcggc gtgcctggcg 600
atgcattga 609

```

<210> 5

<211> 660

<212> DNA

<213> *B. mallei* ATCC 23344 transcriptional regulator gene
bmaR4

<400> 5

```

atgccgttgc cgatccgctg tggcgaaggc ccgtcgcgcg 40
agcagcgcgg tgcgcccggt gcggcccgtc gcccgtcgag 80
aacgctacgt tcggcgacga gaccgggggc gcccggtgag 120
cggacgggtct tgcgggcatg tcctgttcga tcgtcggccg 160
acgcttgctg cgtgcgtgtc gagtccgccc acaatcaccc 200
gcagcgggtct tcagcgggtct ttcggcgcg gcgcctggc 240
ccgccatgag tacgagggcg catggcgag catgttcgag 280
gcctgccggg gcggcgctga gcgtgcgcgg cggcagccgt 320
gatgcagggt tggccggcgc gcgcgggatt cgagcgatgc 360
tcgagcgcgg agcgcgggtt cggcttcggc gcaggcggcc 400
gattgtcccg ccgcgttcga cgaaacgaac ggcgtgccgt 440
gcttcggcgg cgcggcaggc aagctcgccc gcgtttcgcc 480
gcgcgcgggc cgcggttgcc ctctcgcccc ttctgagcac 520
gctttcttca ttggttcgct aacgtaactt cctcacttga 560
gctgggcggg tctatgttcg aaggcttgct cattgggtcg 600
tttaacgaaa ttctgaacgc gacttgcaag aagagcctct 640
ttgagcagac ggcgtatcac 660

```

<210> 6

<211> 726

<212> DNA

<213> *B. mallei* ATCC 23344 transcriptional regulator gene
bmaR5

<400> 6

```

atgagggcgg cgatggggaa ctgggcggag gatctgctgg 40
cggggctcga cagcgcacga tccgaggaag aggcgtttcg 80
aagcgtcgaa accgcggcgg cggcgctcga ttctgaatac 120
tgcgcatacg ggctgcgcgt gccgtggccg ctgtccaggc 160
cgcgcatcga gacgcgcagc aactttcccg agcaatggaa 200
gcggcgctac gtcgagggcg gtttcctcga tgtcgatccg 240
attctcgcgc acggccgcgg atcgcagcaa ccggtcgctc 280
tcgccgagac gctgttttgc tccgcgcacc agatgtgggt 320
cgaggcgcag tcgttcgggt tgcggttcgg ctgggcgcag 360
tcgagcttcg acgcgtatgg cggcatgggc atgctcgcgc 400
tcgtccgctc gcgcgagccg gtgacggcgg cggaactcga 440
cgcgaaggag taccggatgc gctggctcgt gcgcaccgcg 480
cacgccgcgc tcggccgcgt gatgttgccc aagctgatgg 520
cggacccgga gcgcgggctg accgagcgcg aggtcgaggt 560

```

```

gctcaagtgg gggcgggacg gcaagacgtc cggcgagatc 600
tcgaagatcc tcgcatatc cgtcgatacg gtgaatttcc 640
acgtgaagaa cgcgatcctg aagctcagga cggcgaacaa 680
gacggcggcc gtcgtgcgcg cggcgatgct cgggttgctg 720
agctga                                           726

```

<210> 7

<211> 612

<212> DNA

<213> *B. pseudomallei* DD503 AHS gene *bpmI1*

<400> 7

```

atgcgaactt tcgttcatgg cgacggggcg ctgccgagcg 40
acttggcggc tgatctgggc ctttatcggc acggagtttt 80
cgtcgagcag ctcggtctga aactgccgtc ggcaagcgaa 120
gggttcgagc gggatcagta cgatcgcgac gataccgtct 160
atgtgttcgc ccgcgacgac gacggggaaa tctgcggctg 200
cgccccggctg ctgccgacga cccgcccgtg tctgctgaag 240
gaactgttcc cgacgctggg cgcgcaagac atgccgttgc 280
cgcaatccgc cgccgtctgg gaattgtcgc gcttcgccgc 320
gaacgccgag gatccggcgg ggggcggcaa cccggcctgg 360
gcggtgcggc cgatgctcgc cgccgtcgtc gagtgcgccg 400
cgcggtcttg cgcgaaagcaa ctgatcggcg tgacgtttct 440
gagcatggag cgccgtgttc gccggatcgg cgtgcacgcg 480
caccggggcg ggcccgcgca gcagatcgac gggcgcatgg 520
tcgtcgcggt ctggatcgac ctcgacgcgc aaacgctcgc 560
cgcgctcgat ctcgaccgcg tgctgtgcgc gccgcccggc 600
gaagccgcct ga                                           612

```

<210> 8

<211> 621

<212> DNA

<213> *B. pseudomallei* DD503 AHS gene *bpmI2*

<400> 8

```

atgatcgata cgaccgtcat aagcgccgcg caactggatt 40
ccaccgtcaa ggcagcactc ggcaattatc gtcgggcgat 80
attcatcgag aaactcggct ggccattgcc gttggtcgac 120
gggctcgaga tcgatcagtt cgatcgtccc gatacgattt 160
acgtgggtcgg caaaacagag tccggcgata tctgcggatg 200
cgccccgcctg ctgcccacga cgaggcccta cctgctcgga 240
gaggtgttcc ccgatctgat gggcgacgcg gcgcgcgcct 280
gctcggcgca cgtgtgggaa atctcgcgat ttctgtcttc 320
gatcctctcc ggagggccgg acgcgctgcg gcaggctcac 360
cgcaatacgc gcatcctgct cgcgaaaatc gtccgctttg 400
cgcaggcggc cggcgtgaag cggctgatca ccgtttcgcc 440
gctcgcagtc gagcggctgc tcaaccgtct gaaagtccat 480
attcaccgcg cgggtccgcc tcggttgatc gacggcaagc 520
cgggtgttcgc gtgctggatc gaggtggacg acatcacgct 560
ccaagcgctc gacatcgagc cggccgccga ttcggccgcc 600
ggcgcgctgc gccattcgtg a                                           621

```

<210> 9

<211> 609

<212> DNA

<213> *B. pseudomallei* DD503 AHS gene *bpmI3*

<400> 9

atgtcataca	tcacgcgagg	ccgattgaac	gaactgccgc	40
cgcacgtcca	gaccgatctc	ggcgcgtatc	gctacgacgt	80
gttcgtgcgc	cggctcggct	ggacgatcgc	cggccactcg	120
ctcgacgaac	atgcggagtg	ggacgagttc	gacgggccgt	160
cgacgattca	tgctcgtcgc	ctcgacgacg	cgcgcgagat	200
ctgcggctac	gcacgcctgc	tgccgacgac	gggcccgtat	240
ctgctgcgcg	acgtgtttgc	gcatctgctc	ggctcgtcgc	280
ccgcgcgcga	atcgccctgc	gtctgggaaa	tgctcgcgct	320
cgcgcgcgtc	cggcggcggc	gaagcgcgac	cgagcgcgag	360
ccgctcggca	tggcgttctt	tccgtcgggtg	ctcacgggtg	400
ccgcgtcgtc	cggcgcgacg	cgcgtggctc	gcgtgatgac	440
gccatcgatc	gaacgcctgt	accgccgctc	gggcatcgcg	480
ctgcatcgcc	tcggcaacgc	gatgccgggc	gcgggcggca	520
gcctgtccgc	atgctcgatc	gatctgccgc	gcctcgcgtt	560
cgcgccgttg	ggccgcaagc	agtgcgcggc	gtgcctggcg	600
atgcattga				609

<210> 10

<211> 720

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene
bpmR1

<400> 10

atggaactgc	gctggcaaga	cgcctatctt	caatttagcg	40
ccgcggagaa	cgagcagcag	ctcttccaac	agatcgccgc	80
gtatacgaag	cggctcggct	tcgaatattg	ctgctatggc	120
atacgcgtgc	cgttgccgat	ctcgaagccg	gtcgtcgcga	160
ttttcgacac	ctatccgaac	ggctggatgg	agcgtacca	200
ggaaatgaac	tacctggagg	tcgatccgac	cgtacgcgag	240
ggcgcgctca	gctcgaacat	gatcgtcttg	ccggaggcga	280
gcgcgagcga	cgcgacgacg	ctctggagcg	acgcgcgcga	320
tcacgggctg	gcggtcggcg	tcgcgcagtc	gagctggggc	360
tcgcgcgggg	tgttcggctt	cctgacgatc	gcgcggcaca	400
ccgaccgcct	gacgtccgcc	gagatcaacc	atctgacgtt	440
gcaggcgaac	tggctcgcga	acatgtcgca	ctcgtgatg	480
agccgttttc	tcgtgccgaa	gctcgcgccc	gaatcggggc	520
tggcgtcac	gcaccgcgag	cgggaggtgc	tgtgctggac	560
gggggagggc	aagaccgcgt	gcgagatcgg	gcagatcctc	600
agcatctccg	agcgcacggt	gaactttcac	gtcaacaaca	640
tcctcgacaa	gctcggcgcg	acgaacaagg	tcagggccgt	680
cgtgaaggcg	atcgcgatgg	ggctcatcga	cgcgccgtaa	720

<210> 11

<211> 711

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene
bpmR2

<400> 11

atggagatgc	acgactttct	tcaatttttg	ctaaacgaat	40
tttcacgcag	tgagaaccca	cagcacgtca	tttcgctctt	80
gacccgcgcg	gccgcgacgc	tcggctacga	atacgcgcc	120
tacggcatgc	gccgccctt	tccgatcagc	aatccgccga	160
tcctcatggg	gtccaactat	cccgcccgat	ggcaggaacg	200

```

ctatatcgaa ggcgcatcgc cgaacatcga cggcgcggtg 240
aaggccgcgc tcggcagcga ccggcccgtg acctggagcg 280
cgcccgccaa cgcacgcgaa agcgcattct gggcgaggcg 320
gctgtcggtc ggcacgcgcc acggctggtc gtccgcgtcg 360
cggggcgcgg acggcgcgat cggcgtgctg acgctgtcga 400
gaacgcagga cccgatcgac accgcggaga agtttcgcaa 440
cgagagcatc gtgcactggc tcgccaatgt cgctcatgcg 480
tcgatggcgc cgttcctgcc cgccgccgac gagttcgatc 520
cggacctcac ggcgcgcgag accgatgtgc tgaaatggac 560
ggccgacgga aagacagcgt acgaaatcgc gctgattctc 600
agcatctcgg agagcaccgt caattttcac gtgaagaata 640
tcgtctccaa gctgggctcc acgaacaaga tacaggccgt 680
ggccaaggcc gcgctgatgg ggatgctgtg a 711

```

<210> 12

<211> 693

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene
bpmR3

<400> 12

```

atgctctccg ccgcgttgcc ggaatcgcgc gacgtccgca 40
cgctgggtcga gactttcagg caggcggcgc tgcagatcgg 80
ctaccagcac catgcgatcg tcgagctgtc gggcgcatcg 120
catccggcgt cgatcgacgt cgtctcgctg cactatccgt 160
ccgagtgggt cgagcactac acccgcaacg actacttcgc 200
gatcgatccc gtccatcgcg cggcattccg ctacagcacg 240
ccgttctcgt ggaacgacgt cgcgacggcg aacctgcgcg 280
agcggcatct gctgatggaa gccgaggacg cgggcctcga 320
caacggcatc agcatccgcg tgcatcagcc gctcggacgc 360
gtgctgctgg tgagcctgtc cggcaccgcg ccgacgcacg 400
atgccgatgc gaaatggcgc aacgcgtacc tgctcggcat 440
gcagttcaat ctgcagttcc agagcatgcg cacgtgccgc 480
ccgattccgc cgtccgtcca cctgacggat cgcgaacaga 520
tgtgcctcac gtgggtcgcg cgcggcaagt cgtcgtgggt 560
catcgcgaac atgctcgaca tctccaaata cacggtcgac 600
ttccacatcg agaacgcgat ggagaagctc aacacgcgca 640
gccgcacgtt cgccgccgtg aaggcgacgc ggcaggggct 680
catctttcca tga 693

```

<210> 13

<211> 885

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene
bpmR4

<400> 13

```

atggcgcgaa cgcgccgagg ggcaagcgaa tcgcgccgca 40
gcgcgcgcgc cggcgcgata gccgcgcgac ctgcgttccg 80
cgcccgccgc acaggcgggt cgccgcgcgg tcgcgcgcaa 120
ccgcttgccg gcggcgggcg cgcgcgctca gatcaaccgc 160
cgcgccgatg cgatgacgac cgcttgcgcg cggttgttcg 200
cgcctatctt gcgtgcggcg ttcgacagat gaaacacgac 240
cgtgcgctcc gagatgccga gaatcttcga gatttccac 280
gccgtcttgc cgcgccccgc ccaactgcagc gattcgcgct 320
cgcgcgcggt cagatcgcac gagccctgcc gtctgagccg 360

```

```

gcaatcgagc agctcgtgca tcgccgcgtg cacgaagctc 400
gcgagcaact gcgacaggct cagcagccgc agtatgtcgc 440
tcgcgtcgtg ctggaacgga tcgtcggtcg ccatgctgag 480
catgctgata gcgccgctgc gatcgtgaac ggggcaactg 520
agcccgtaga cgaggccgta cgatttcgcc tcgtcgcgca 560
tgagcttcgc gcggctggtc gtatagaggt cgtcgtgcca 600
gatgagcggc acggtccggc accggcaatg ctgaacgacg 640
ggatcgatcg acaggtagtc ggccggcgtc tagcgcagcc 680
gccactcggc cggaaatccg tcgagcatgc agcggctcga 720
cgccgcgcgc gagatctgat gccggtacgc gaaattcttg 760
aagcccagtt ggcgaacgtg atacgccgtc tgctcaaaga 800
ggctcttctt gcaagtgcgc ttcagaattt cgttaaacga 840
accaatggac aagccttcga acatagaacc gcccagctca 880
agtga 885

```

<210> 14

<211> 726

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene
bpmR5

<400> 14

```

atgagggcgg cgatggggaa ctgggcggag gatctgctgg 40
cggggctcga cagcgcacga tccgaggaag aggcgtttcg 80
aagcgtcgaa accgcggcgg cggcgctcga tttcgaatac 120
tgcgcatacg ggctgcgcgt gccgtggccg ctgtccaggc 160
cgcgcatcga gacgcgcagc aactttcccg agcaatggaa 200
gcggcgctac gtcgaggcgg gtttcctcga cgtcgatccg 240
attctcgcgc acggccgcgc atcgcagcaa ccggtcgtcc 280
tcgccgagac gctgttttgcg tccgcgcacc agatgtgggt 320
cgaggcgcag tcgttcgggt tgcggttcgg ctgggcgcag 360
tcgagcttcg acgcgtatgg cggcatgggc atgctcgcgc 400
tcgtccgctc gtgcgagccg gtgacggcgg cggaactcga 440
cgcgaaggag taccggatgc gctggctcgt gcgcaccgcg 480
cacgccgcgc tcggccgcac gatgttgccc aagctgatgg 520
cggaccgcga gcgcgggctg accgagcgcg aggtcagagg 560
gctcaagtgg gcggcggacg gcaagacgtc cggcgagatc 600
tcgaagatcc tcgcgatatc cgtcgatacg gtgaatttcc 640
acgtgaagaa cgcgatcctg aagctcagga cggcgaacaa 680
gacggcggcc gtcgtgcgcg cggcgatgct cggggttgctg 720
agctga 726

```

<210> 15

<211> 203

<212> PRT

<213> *B. mallei* ATCC 23344 bmaI1

<400> 15

```

Met Arg Thr Phe Val His Gly Asp Gly Arg
 1             5             10
Leu Pro Ser Asp Leu Ala Ala Ala Leu Gly
             15             20
Leu Tyr Arg His Gly Val Phe Val Glu Gln
             25             30
Leu Gly Trp Lys Leu Pro Ser Ala Ser Glu

```

				35					40
Gly	Phe	Glu	Arg	Asp	Gln	Tyr	Asp	Arg	Asp
				45					50
Asp	Thr	Val	Tyr	Val	Phe	Ala	Arg	Asp	Asp
				55					60
Gly	Glu	Ile	Cys	Gly	Cys	Ala	Arg	Leu	Leu
				65					70
Pro	Thr	Thr	Arg	Pro	Tyr	Leu	Leu	Lys	Glu
				75					80
Lys	Phe	Pro	Thr	Leu	Val	Ala	Gln	Asp	Met
				85					90
Pro	Leu	Pro	Gln	Ser	Ala	Ala	Val	Trp	Glu
				95					100
Leu	Ser	Arg	Phe	Ala	Ala	Asn	Ala	Glu	Asp
				105					110
Pro	Ala	Gly	Gly	Gly	Asn	Pro	Ala	Trp	Ala
				115					120
Val	Arg	Pro	Met	Leu	Ala	Ala	Val	Val	Glu
				125					130
Cys	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Gln	Leu
				135					140
Ile	Gly	Val	Thr	Phe	Leu	Ser	Met	Glu	Arg
				145					150
Leu	Phe	Arg	Arg	Ile	Gly	Val	His	Ala	His
				155					160
Arg	Ala	Gly	Pro	Ala	Gln	Gln	Ile	Asp	Gly
				165					170
Arg	Met	Val	Val	Ala	Cys	Trp	Ile	Asp	Leu
				175					180
Asp	Ala	Gln	Thr	Leu	Ala	Ala	Leu	Asp	Leu
				185					190
Asp	Leu	Pro	Leu	Leu	Cys	Ala	Pro	Pro	Ala
				195					200
Glu	Ala	Ala							

<210> 16

<211> 202

<212> PRT

<213> *B. mallei* ATCC 23344 bmaI3

<400> 16

Met	Ser	Tyr	Ile	Ile	Ala	Gly	Arg	Leu	Asn
1				5					10
Glu	Lys	Pro	Pro	His	Val	Gln	Thr	Asp	Leu
				15					20
Gly	Ala	Tyr	Arg	Tyr	Asp	Val	Phe	Val	Arg
				25					30
Arg	Leu	Gly	Trp	Thr	Ile	Ala	Gly	His	Ser
				35					40
Leu	Asp	Glu	His	Ala	Glu	Trp	Asp	Glu	Phe
				45					50
Asp	Gly	Pro	Ser	Thr	Ile	His	Val	Val	Ala
				55					60
Leu	Asp	Asp	Ala	Arg	Glu	Ile	Cys	Gly	Tyr

				65					70
Ala	Arg	Leu	Leu	Pro	Thr	Thr	Gly	Pro	Tyr
				75					80
Leu	Leu	Arg	Asp	Val	Phe	Ala	His	Leu	Leu
				85					90
Gly	Ser	Ser	Pro	Ala	Pro	Gln	Ser	Pro	Ala
				95					100
Val	Trp	Glu	Met	Ser	Arg	Phe	Ala	Ala	Ser
				105					110
Arg	Arg	Arg	Arg	Ser	Ala	Thr	Glu	Arg	Glu
				115					120
Pro	Leu	Gly	Met	Ala	Phe	Phe	Pro	Ser	Val
				125					130
Leu	Thr	Val	Ala	Ala	Ser	Leu	Gly	Ala	Thr
				135					140
Arg	Val	Val	Gly	Val	Met	Thr	Pro	Ser	Ile
				145					150
Glu	Arg	Leu	Tyr	Arg	Arg	Ser	Gly	Ile	Ala
				155					160
Leu	His	Arg	Leu	Gly	Asn	Ala	Met	Pro	Gly
				165					170
Ala	Gly	Gly	Ser	Leu	Ser	Ala	Cys	Ser	Ile
				175					180
Asp	Leu	Pro	Arg	Leu	Ala	Phe	Ala	Pro	Leu
				185					190
Gly	Leu	Lys	Gln	Cys	Ala	Ala	Cys	Leu	Ala
				195					200
Met	His								

<210> 17

<211> 239

<212> PRT

<213> *B. mallei* ATCC 23344 bmaR1

<400> 17

Met	Glu	Leu	Arg	Trp	Gln	Asp	Ala	Tyr	Leu
1				5					10
Gln	Phe	Ser	Ala	Ala	Glu	Asn	Glu	Gln	Gln
				15					20
Leu	Phe	Gln	Gln	Ile	Ala	Ala	Tyr	Thr	Lys
				25					30
Arg	Leu	Gly	Phe	Glu	Tyr	Cys	Cys	Tyr	Gly
				35					40
Ile	Arg	Val	Pro	Leu	Pro	Ile	Ser	Lys	Pro
				45					50
Val	Val	Ala	Ile	Phe	Asp	Thr	Tyr	Pro	Asn
				55					60
Gly	Trp	Met	Glu	Arg	Tyr	Gln	Glu	Met	Asn
				65					70
Tyr	Leu	Glu	Val	Asp	Pro	Thr	Val	Arg	Glu
				75					80
Gly	Ala	Leu	Ser	Ser	Asn	Met	Ile	Val	Trp
				85					90
Pro	Glu	Ala	Ser	Ala	Ser	Asp	Ala	Thr	Thr

```

          95                                100
Leu Trp Ser Asp Ala Arg Asp His Gly Leu
          105                                110
Ala Val Gly Val Ala Gln Ser Ser Trp Ala
          115                                120
Ser Arg Gly Val Phe Gly Leu Leu Thr Ile
          125                                130
Ala Arg His Thr Asp Arg Leu Thr Ser Ala
          135                                140
Glu Ile Asn His Leu Thr Leu Gln Ala Asn
          145                                150
Trp Leu Ala Asn Met Ser His Ser Leu Met
          155                                160
Ser Arg Phe Leu Val Pro Lys Leu Ala Pro
          165                                170
Glu Ser Gly Val Ala Leu Thr His Arg Glu
          175                                180
Arg Glu Val Leu Cys Trp Thr Gly Glu Gly
          185                                190
Lys Thr Ala Cys Glu Ile Gly Gln Ile Leu
          195                                200
Ser Ile Ser Glu Arg Thr Val Asn Phe His
          205                                210
Val Asn Asn Ile Leu Asp Lys Leu Gly Ala
          215                                220
Thr Asn Lys Val Gln Ala Val Val Lys Ala
          225                                230
Ile Ala Met Gly Leu Ile Asp Ala Pro
          235

```

<210> 18

<211> 202

<212> PRT

<213> *B. mallei* ATCC 23344 bmaR3

<400> 18

```

Met Ser Tyr Ile Ile Ala Gly Arg Leu Asn
  1          5                                10
Glu Leu Pro Pro His Val Gln Thr Asp Leu
          15                                20
Gly Ala Tyr Arg Tyr Asp Val Phe Val Arg
          25                                30
Arg Leu Gly Trp Thr Ile Ala Gly His Ser
          35                                40
Leu Asp Glu His Ala Glu Trp Asp Glu Phe
          45                                50
Asp Gly Pro Ser Thr Ile His Val Val Ala
          55                                60
Leu Asp Asp Ala Arg Glu Ile Cys Gly Tyr
          65                                70
Ala Arg Leu Leu Pro Thr Thr Gly Pro Tyr
          75                                80
Leu Leu Arg Asp Val Phe Ala His Leu Leu
          85                                90
Gly Ser Ser Pro Ala Pro Gln Ser Pro Ala

```

				95					100
Val	Trp	Glu	Met	Ser	Arg	Phe	Ala	Ala	Ser
				105					110
Arg	Arg	Arg	Arg	Ser	Ala	Thr	Glu	Arg	Glu
				115					120
Pro	Leu	Gly	Met	Ala	Phe	Phe	Pro	Ser	Val
				125					130
Leu	Thr	Val	Ala	Ala	Ser	Leu	Gly	Ala	Thr
				135					140
Arg	Val	Val	Gly	Val	Met	Thr	Pro	Ser	Ile
				145					150
Glu	Arg	Leu	Tyr	Arg	Arg	Ser	Gly	Ile	Ala
				155					160
Leu	His	Arg	Leu	Gly	Asn	Ala	Met	Pro	Gly
				165					170
Ala	Gly	Gly	Ser	Leu	Ser	Ala	Cys	Ser	Ile
				175					180
Asp	Leu	Pro	Arg	Leu	Ala	Phe	Ala	Pro	Leu
				185					190
Gly	Leu	Lys	Gln	Cys	Ala	Ala	Cys	Leu	Ala
				195					200
Met	His								

<210> 19

<211> 220

<212> PRT

<213> *B. mallei* ATCC 23344 bmaR4

<400> 19

Met	Pro	Leu	Pro	Ile	Arg	Cys	Gly	Glu	Gly
1				5					10
Pro	Ser	Pro	Gln	Gln	Arg	Gly	Ala	Pro	Arg
				15					20
Ala	Ala	Arg	Arg	Pro	Ser	Arg	Thr	Leu	Arg
				25					30
Ser	Ala	Thr	Arg	Pro	Gly	Ala	Pro	Arg	Ala
				35					40
Arg	Thr	Val	Leu	Arg	Ala	Cys	Pro	Val	Arg
				45					50
Ser	Ser	Ala	Asp	Ala	Cys	Val	Val	Arg	Val
				55					60
Glu	Ser	Ala	Asp	Asn	His	Pro	Gln	Arg	Ser
				65					70
Ser	Ala	Val	Phe	Arg	Arg	Ala	Thr	Pro	Gly
				75					80
Pro	Pro	Cys	Val	Arg	Gly	Arg	Met	Ala	Gln
				85					90
His	Val	Arg	Gly	Leu	Pro	Gly	Arg	Arg	Arg
				95					100
Ala	Cys	Ala	Ala	Ala	Ala	Val	Met	Gln	Val
				105					110
Trp	Pro	Ala	Arg	Ala	Gly	Phe	Glu	Arg	Cys
				115					120
Ser	Ser	Ala	Glu	Arg	Arg	Phe	Gly	Phe	Gly

				125					130
Ala	Gly	Gly	Arg	Leu	Ser	Arg	Arg	Val	Arg
				135					140
Arg	Asn	Glu	Arg	Arg	Ala	Val	Leu	Arg	Arg
				145					150
Arg	Gly	Arg	Gln	Ala	Arg	Arg	Arg	Phe	Ala
				155					160
Ala	Arg	Gly	Pro	Pro	Leu	Pro	Ser	Arg	Pro
				165					170
Phe	Arg	Ala	Arg	Phe	Leu	His	Trp	Phe	Ala
				175					180
Asn	Val	Thr	Ser	Ser	Leu	Glu	Leu	Gly	Gly
				185					190
Ser	Met	Phe	Glu	Gly	Leu	Ser	Ile	Gly	Ser
				195					200
Phe	Asn	Glu	Ile	Leu	Asn	Ala	Thr	Cys	Lys
				205					210
Lys	Ser	Leu	Phe	Glu	Gln	Thr	Ala	Tyr	His
				215					220

<210> 20

<211> 241

<212> PRT

<213> *B. mallei* ATCC 23344 bmaR5

<400> 20

Met	Arg	Ala	Ala	Met	Gly	Asn	Trp	Ala	Glu
1				5					10
Asp	Leu	Leu	Ala	Gly	Leu	Asp	Ser	Ala	Arg
				15					20
Ser	Glu	Glu	Glu	Arg	Phe	Arg	Ser	Val	Glu
				25					30
Thr	Ala	Ala	Ala	Ala	Leu	Asp	Phe	Glu	Tyr
				35					40
Cys	Ala	Tyr	Gly	Leu	Arg	Val	Pro	Trp	Pro
				45					50
Leu	Ser	Arg	Pro	Arg	Ile	Glu	Thr	Arg	Ser
				55					60
Asn	Phe	Pro	Glu	Gln	Trp	Lys	Arg	Arg	Tyr
				65					70
Val	Glu	Ala	Gly	Phe	Leu	Asp	Val	Asp	Pro
				75					80
Ile	Leu	Ala	His	Gly	Arg	Arg	Ser	Gln	Gln
				85					90
Pro	Val	Val	Leu	Ala	Glu	Thr	Leu	Phe	Ala
				95					100
Ser	Ala	His	Gln	Met	Trp	Val	Glu	Ala	Gln
				105					110
Ser	Phe	Gly	Leu	Arg	Phe	Gly	Trp	Ala	Gln
				115					120
Ser	Ser	Phe	Asp	Ala	Tyr	Gly	Gly	Met	Gly
				125					130
Met	Leu	Ala	Leu	Val	Arg	Ser	Arg	Glu	Pro
				135					140

Val	Thr	Ala	Ala	Glu	Leu	Asp	Ala	Lys	Glu	
				145					150	
Tyr	Arg	Met	Arg	Trp	Leu	Val	Arg	Thr	Ala	
				155					160	
His	Ala	Ala	Leu	Gly	Arg	Met	Met	Leu	Pro	
				165					170	
Lys	Leu	Met	Ala	Asp	Pro	Glu	Arg	Glu	Leu	
				175					180	
Thr	Glu	Arg	Glu	Val	Glu	Val	Leu	Lys	Trp	
				185					190	
Ala	Ala	Asp	Gly	Lys	Thr	Ser	Gly	Glu	Ile	
				195					200	
Ser	Lys	Ile	Leu	Ala	Ile	Ser	Val	Asp	Thr	
				205					210	
Val	Asn	Phe	His	Val	Lys	Asn	Ala	Ile	Leu	
				215					220	
Lys	Leu	Arg	Thr	Ala	Asn	Lys	Thr	Ala	Ala	
				225					230	
Val	Val	Arg	Ala	Ala	Met	Leu	Gly	Leu	Leu	
				235					240	

Ser

<210> 21
 <211> 203
 <212> PRT
 <213> *B. pseudomallei* DD503 bpmI1
 <400> 21

Met	Arg	Thr	Phe	Val	His	Gly	Asp	Gly	Arg	
1				5					10	
Leu	Pro	Ser	Asp	Leu	Ala	Ala	Asp	Leu	Gly	
				15					20	
Leu	Tyr	Arg	His	Gly	Val	Phe	Val	Glu	Gln	
				25					30	
Leu	Gly	Trp	Lys	Leu	Pro	Ser	Ala	Ser	Glu	
				35					40	
Gly	Phe	Glu	Arg	Asp	Gln	Tyr	Asp	Arg	Asp	
				45					50	
Asp	Thr	Val	Tyr	Val	Phe	Ala	Arg	Asp	Asp	
				55					60	
Asp	Gly	Glu	Ile	Cys	Gly	Cys	Ala	Arg	Leu	
				65					70	
Leu	Pro	Thr	Thr	Arg	Pro	Tyr	Leu	Leu	Lys	
				75					80	
Glu	Leu	Glu	Pro	Thr	Leu	Val	Ala	Gln	Asp	
				85					90	
Met	Pro	Leu	Pro	Gln	Ser	Ala	Ala	Val	Trp	
				95					100	
Glu	Leu	Ser	Arg	Phe	Ala	Ala	Asn	Ala	Glu	
				105					110	
Asp	Pro	Ala	Gly	Gly	Gly	Asn	Pro	Ala	Trp	
				115					120	
Ala	Val	Arg	Pro	Met	Leu	Ala	Ala	Val	Val	
				125					130	

Glu	Cys	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Gln	
				135					140	
Leu	Ile	Gly	Val	Thr	Phe	Leu	Ser	Met	Glu	
				145					150	
Arg	Leu	Phe	Arg	Arg	Ile	Gly	Val	His	Ala	
				155					160	
His	Arg	Ala	Gly	Pro	Ala	Gln	Gln	Ile	Asp	
				165					170	
Gly	Arg	Met	Val	Val	Ala	Cys	Trp	Ile	Asp	
				175					180	
Leu	Asp	Ala	Gln	Thr	Leu	Ala	Ala	Leu	Asp	
				185					190	
Leu	Asp	Pro	Leu	Leu	Cys	Ala	Pro	Pro	Ala	
				195					200	
Glu	Ala	Ala								

<210> 22

<211> 206

<212> PRT

<213> *B. pseudomallei* DD503 bpmI2

<400> 22

Met	Ile	Asp	Thr	Thr	Val	Ile	Ser	Ala	Ala	
1				5					10	
Gln	Leu	Asp	Ser	Thr	Val	Lys	Ala	Ala	Leu	
				15					20	
Gly	Asn	Tyr	Arg	Arg	Ala	Ile	Phe	Ile	Glu	
				25					30	
Lys	Leu	Gly	Trp	Pro	Leu	Pro	Leu	Val	Asp	
				35					40	
Gly	Leu	Glu	Ile	Asp	Gln	Phe	Asp	Arg	Pro	
				45					50	
Asp	Thr	Ile	Tyr	Val	Val	Gly	Lys	Thr	Glu	
				55					60	
Ser	Gly	Asp	Ile	Cys	Gly	Cys	Ala	Arg	Leu	
				65					70	
Leu	Pro	Thr	Thr	Arg	Pro	Tyr	Leu	Leu	Gly	
				75					80	
Glu	Val	Phe	Pro	Asp	Leu	Met	Gly	Asp	Ala	
				85					90	
Ala	Pro	Pro	Cys	Ser	Ala	His	Val	Trp	Glu	
				95					100	
Ile	Ser	Arg	Phe	Ser	Ser	Ser	Ile	Leu	Ser	
				105					110	
Gly	Gly	Pro	Asp	Ala	Leu	Arg	Gln	Ala	His	
				115					120	
Arg	Asn	Thr	Arg	Ile	Leu	Leu	Ala	Lys	Ile	
				125					130	
Val	Arg	Phe	Ala	Gln	Ala	Ala	Gly	Val	Lys	
				135					140	
Arg	Leu	Ile	Thr	Val	Ser	Pro	Leu	Ala	Val	
				145					150	
Glu	Arg	Leu	Leu	Asn	Arg	Leu	Lys	Val	His	
				155					160	

Ile	His	Arg	Ala	Gly	Pro	Pro	Arg	Leu	Ile	
				165					170	
Asp	Gly	Lys	Pro	Val	Phe	Ala	Cys	Gln	Ile	
				175					180	
Glu	Val	Asp	Asp	Ile	Thr	Leu	Gln	Ala	Leu	
				185					190	
Asp	Ile	Glu	Pro	Ala	Ala	Asp	Ser	Ala	Ala	
				195					200	
Gly	Ala	Leu	Arg	His	Ser					
				205						

<210> 23

<211> 202

<212> PRT

<213> *B. pseudomallei* DD503 bpmI3

<400> 23

Met	Ser	Tyr	Ile	Ile	Ala	Gly	Arg	Leu	Asn	
1				5					10	
Glu	Leu	Pro	Pro	His	Val	Gln	Thr	Asp	Leu	
				15					20	
Gly	Ala	Tyr	Arg	Tyr	Asp	Val	Phe	Val	Arg	
				25					30	
Arg	Leu	Gly	Trp	Thr	Ile	Ala	Gly	His	Ser	
				35					40	
Leu	Asp	Glu	His	Ala	Glu	Trp	Asp	Glu	Phe	
				45					50	
Asp	Gly	Pro	Ser	Thr	Ile	His	Val	Val	Ala	
				55					60	
Leu	Asp	Asp	Ala	Arg	Glu	Ile	Cys	Gly	Tyr	
				65					70	
Ala	Arg	Leu	Leu	Pro	Thr	Thr	Gly	Pro	Tyr	
				75					80	
Leu	Leu	Arg	Asp	Val	Phe	Ala	His	Leu	Leu	
				85					90	
Gly	Ser	Ser	Pro	Ala	Pro	Gln	Ser	Pro	Ala	
				95					100	
Val	Trp	Glu	Met	Ser	Arg	Phe	Ala	Ala	Ser	
				105					110	
Arg	Arg	Arg	Arg	Ser	Ala	Thr	Glu	Arg	Glu	
				115					120	
Pro	Leu	Gly	Met	Ala	Phe	Phe	Pro	Ser	Val	
				125					130	
Leu	Thr	Val	Ala	Ala	Ser	Leu	Gly	Ala	Thr	
				135					140	
Arg	Val	Val	Gly	Val	Met	Thr	Pro	Ser	Ile	
				145					150	
Glu	Arg	Leu	Tyr	Arg	Arg	Ser	Gly	Ile	Ala	
				155					160	
Leu	His	Arg	Leu	Gly	Asn	Ala	Met	Pro	Gly	
				165					170	
Ala	Gly	Gly	Ser	Leu	Ser	Ala	Cys	Ser	Ile	
				175					180	
Asp	Leu	Pro	Arg	Leu	Ala	Phe	Ala	Pro	Leu	
				185					190	

Gly Arg Lys Gln Cys Ala Ala Cys Leu Ala
 195 200
 Met. His

<210> 24
 <211> 239
 <212> PRT
 <213> *B. pseudomallei* DD503 bpmR1
 <400> 24

Met	Glu	Leu	Arg	Trp	Gln	Asp	Ala	Tyr	Leu	
1				5					10	
Gln	Phe	Ser	Ala	Ala	Glu	Asn	Glu	Gln	Gln	
				15					20	
Leu	Phe	Gln	Gln	Ile	Ala	Ala	Tyr	Thr	Lys	
				25					30	
Arg	Leu	Gly	Phe	Glu	Tyr	Cys	Cys	Tyr	Gly	
				35					40	
Ile	Arg	Val	Pro	Leu	Pro	Ile	Ser	Lys	Pro	
				45					50	
Val	Val	Ala	Ile	Phe	Asp	Thr	Tyr	Pro	Asn	
				55					60	
Gly	Trp	Met	Glu	Arg	Tyr	Gln	Glu	Met	Asn	
				65					70	
Tyr	Leu	Glu	Val	Asp	Pro	Thr	Val	Arg	Glu	
				75					80	
Gly	Ala	Leu	Ser	Ser	Asn	Met	Ile	Val	Trp	
				85					90	
Pro	Glu	Ala	Ser	Ala	Ser	Asp	Ala	Thr	Thr	
				95					100	
Leu	Trp	Ser	Asp	Ala	Arg	Asp	His	Gly	Leu	
				105					110	
Ala	Val	Gly	Val	Ala	Gln	Ser	Ser	Trp	Ala	
				115					120	
Ser	Arg	Gly	Val	Phe	Gly	Leu	Leu	Thr	Ile	
				125					130	
Ala	Arg	His	Thr	Asp	Arg	Leu	Thr	Ser	Ala	
				135					140	
Glu	Ile	Asn	His	Leu	Thr	Leu	Gln	Ala	Asn	
				145					150	
Trp	Leu	Ala	Asn	Met	Ser	His	Ser	Leu	Met	
				155					160	
Ser	Arg	Phe	Leu	Val	Pro	Lys	Leu	Ala	Pro	
				165					170	
Glu	Ser	Gly	Val	Ala	Leu	Thr	His	Arg	Glu	
				175					180	
Arg	Glu	Val	Leu	Cys	Trp	Thr	Gly	Glu	Gly	
				185					190	
Lys	Thr	Ala	Cys	Glu	Ile	Gly	Gln	Ile	Leu	
				195					200	
Ser	Ile	Ser	Glu	Arg	Thr	Val	Asn	Phe	His	
				205					210	
Val	Asn	Asn	Ile	Leu	Asp	Lys	Leu	Gly	Ala	
				215					220	

Thr Asn Lys Val Gln Ala Val Val Lys Ala
 225 230
 Ile Ala Met Gly Leu Ile Asp Ala Pro
 235

<210> 25

<211> 236

<212> PRT

<213> *B. pseudomallei* DD503 bpmR2

<400> 25

Met Glu Met His Asp Phe Leu Gln Phe Trp
 1 5 10
 Leu Asn Glu Phe Ser Arg Ser Glu Asn Pro
 15 20
 Gln His Val Ile Ser Val Leu Thr Arg Ala
 25 30
 Ala Ala Thr Leu Gly Tyr Glu Tyr Ala Ala
 35 40
 Tyr Gly Met Arg Arg Pro Phe Pro Ile Ser
 45 50
 Asn Pro Pro Ile Leu Met Val Ser Asn Tyr
 55 60
 Pro Ala Arg Trp Gln Glu Arg Tyr Ile Glu
 65 70
 Ala Arg Phe Ala Asn Ile Asp Gly Ala Val
 75 80
 Lys Ala Ala Leu Gly Ser Asp Arg Pro Val
 85 90
 Thr Trp Ser Ala Pro Ala Asn Ala Ser Lys
 95 100
 Ser Ala Phe Trp Ala Glu Ala Leu Ser Phe
 105 110
 Gly Ile Ala His Gly Trp Ser Ser Ala Ser
 115 120
 Arg Gly Ala Asp Gly Ala Ile Gly Val Leu
 125 130
 Thr Leu Ser Arg Thr Gln Asp Pro Ile Asp
 135 140
 Thr Ala Glu Lys Phe Arg Asn Glu Ser Ile
 145 150
 Val His Trp Leu Ala Asn Val Ala His Ala
 155 160
 Ser Met Ala Pro Phe Leu Pro Ala Ala Asp
 165 170
 Glu Phe Asp Pro Asp Leu Thr Arg Arg Glu
 175 180
 Thr Asp Val Leu Lys Trp Thr Ala Asp Gly
 185 190
 Lys Thr Ala Tyr Glu Ile Ala Leu Ile Leu
 195 200
 Ser Ile Ser Glu Ser Thr Val Asn Phe His
 205 210
 Val Lys Asn Ile Val Ser Lys Leu Gly Ser
 215 220

```

Thr Asn Lys Ile Gln Ala Val Ala Lys Ala
      225                      230
Ala Leu Met Gly Met Leu
      235

```

<210> 26

<211> 230

<212> PRT

<213> *B. pseudomallei* DD503 bpmR3

<400> 26

Met	Leu	Ser	Ala	Ala	Leu	Pro	Glu	Ser	Arg
1				5					10
Asp	Val	Arg	Thr	Leu	Val	Glu	Thr	Phe	Arg
				15					20
Gln	Ala	Ala	Leu	Gln	Ile	Gly	Tyr	Gln	His
				25					30
His	Ala	Ile	Val	Glu	Leu	Ser	Gly	Ala	Ser
				35					40
His	Pro	Ala	Ser	Ile	Asp	Val	Val	Ser	Leu
				45					50
His	Tyr	Pro	Ser	Glu	Trp	Val	Glu	His	Tyr
				55					60
Thr	Arg	Asn	Asp	Tyr	Phe	Ala	Ile	Asp	Pro
				65					70
Val	His	Arg	Ala	Ala	Phe	Arg	Tyr	Ser	Thr
				75					80
Pro	Phe	Ser	Trp	Asn	Asp	Val	Ala	Thr	Ala
				85					90
Asn	Leu	Arg	Glu	Arg	His	Leu	Leu	Met	Glu
				95					100
Ala	Glu	Asp	Ala	Gly	Leu	Asp	Asn	Gly	Ile
				105					110
Ser	Ile	Pro	Leu	His	Gln	Pro	Leu	Gly	Arg
				115					120
Val	Leu	Leu	Val	Ser	Leu	Ser	Gly	Thr	Ala
				125					130
Pro	Thr	His	Asp	Ala	Asp	Ala	Lys	Trp	Arg
				135					140
Asn	Ala	Tyr	Leu	Leu	Gly	Met	Gln	Phe	Asn
				145					150
Leu	Gln	Phe	Gln	Ser	Met	Arg	Thr	Cys	Arg
				155					160
Pro	Ile	Pro	Pro	Ser	Val	His	Leu	Thr	Asp
				165					170
Arg	Glu	Gln	Met	Cys	Leu	Thr	Trp	Val	Ala
				175					180
Arg	Gly	Lys	Ser	Ser	Trp	Val	Ile	Ala	Asn
				185					190
Met	Leu	Asp	Ile	Ser	Lys	Tyr	Thr	Val	Asp
				195					200
Phe	His	Ile	Glu	Asn	Ala	Met	Glu	Lys	Leu
				205					210
Asn	Thr	Arg	Ser	Arg	Thr	Phe	Ala	Ala	Val
				215					220

Lys Ala Thr Arg Gln Glu Leu Ile Phe Pro
225 230

<210> 27

<211> 294

<212> PRT

<213> *B. pseudomallei* DD503 bpmR4

<400> 27

Met	Ala	Arg	Thr	Arg	Arg	Gly	Ala	Ser	Glu
1				5					10
Ser	Arg	Arg	Ser	Ala	Arg	Ala	Gly	Ala	Ile
				15					20
Ala	Ala	Arg	Pro	Ala	Phe	Arg	Ala	Arg	Arg
				25					30
Thr	Gly	Gly	Ser	Pro	Arg	Gly	Arg	Ala	Gln
				35					40
Pro	Leu	Ala	Arg	Gly	Gly	Gly	Ala	Arg	Ser
				45					50
Asp	Gln	Pro	Ala	Arg	Arg	Cys	Asp	Asp	Asp
				55					60
Arg	Leu	Arg	Ala	Val	Val	Arg	Ala	Tyr	Leu
				65					70
Ala	Cys	Gly	Val	Arg	Gln	Met	Lys	His	Asp
				75					80
Arg	Ala	Leu	Arg	Asp	Ala	Glu	Asn	Leu	Arg
				85					90
Asp	Phe	Pro	Arg	Arg	Leu	Ala	Ala	Pro	Arg
				95					100
Pro	Leu	Gln	Arg	Phe	Ala	Leu	Ala	Arg	Gly
				105					110
Gln	Ile	Ala	Arg	Ala	Leu	Pro	Ser	Glu	Pro
				115					120
Ala	Ile	Glu	Gln	Leu	Val	His	Arg	Arg	Val
				125					130
His	Glu	Ala	Arg	Glu	Gln	Leu	Arg	Gln	Ala
				135					140
Gln	Gln	Pro	Gln	Tyr	Val	Ala	Arg	Val	Val
				145					150
Leu	Glu	Arg	Ile	Val	Gly	Arg	His	Ala	Glu
				155					160
His	Ala	Asp	Arg	Ala	Ala	Ala	Ile	Val	Asn
				165					170
Gly	Ala	Thr	Glu	Pro	Val	Asp	Glu	Ala	Val
				175					180
Arg	Phe	Arg	Leu	Val	Ala	His	Glu	Leu	Arg
				185					190
Ala	Ala	Gly	Arg	Ile	Glu	Val	Val	Val	Pro
				195					200
Asp	Glu	Arg	His	Gly	Pro	Ala	Pro	Ala	Met
				205					210
Leu	Asn	Asp	Gly	Ile	Asp	Arg	Gln	Val	Val
				215					220
Gly	Gly	Val	Val	Ala	Gln	Pro	Pro	Leu	Gly
				225					230

Arg	Lys	Ser	Val	Glu	His	Ala	Ala	Ala	Arg
				235					240
Arg	Arg	Ala	Gly	Asp	Leu	Met	Pro	Val	Arg
				245					250
Glu	Ile	Leu	Glu	Ala	Gln	Leu	Ala	Asn	Val
				255					260
Ile	Arg	Arg	Leu	Leu	Lys	Glu	Ala	Leu	Leu
				265					270
Asn	Ser	Arg	Val	Gln	Asn	Phe	Val	Lys	Arg
				275					280
Thr	Asn	Gly	Gln	Ala	Phe	Glu	His	Arg	Thr
				285					290
Ala	Gln	Leu	Lys						

<210> 28

<211> 241

<212> PRT

<213> *B. pseudomallei* DD503 bpmR5

<400> 28

Met	Arg	Ala	Ala	Met	Gly	Asn	Trp	Ala	Glu
1				5					10
Asp	Leu	Leu	Ala	Gly	Leu	Asp	Ser	Ala	Arg
				15					20
Ser	Glu	Glu	Glu	Ala	Phe	Arg	Ser	Val	Glu
				25					30
Thr	Ala	Ala	Ala	Ala	Leu	Asp	Phe	Glu	Tyr
				35					40
Cys	Ala	Tyr	Gly	Leu	Arg	Val	Pro	Trp	Pro
				45					50
Leu	Ser	Arg	Pro	Arg	Ile	Glu	Thr	Arg	Ser
				55					60
Asn	Phe	Pro	Glu	Gln	Trp	Lys	Arg	Arg	Tyr
				65					70
Val	Glu	Ala	Gly	Phe	Leu	Asp	Val	Asp	Pro
				75					80
Ile	Leu	Ala	His	Gly	Arg	Arg	Ser	Gln	Gln
				85					90
Pro	Val	Val	Leu	Ala	Glu	Thr	Leu	Phe	Ala
				95					100
Ser	Ala	His	Gln	Met	Trp	Val	Glu	Ala	Gln
				105					110
Ser	Phe	Gly	Leu	Arg	Phe	Gly	Trp	Ala	Gln
				115					120
Ser	Ser	Phe	Asp	Ala	Tyr	Gly	Gly	Met	Gly
				125					130
Met	Leu	Ala	Leu	Val	Arg	Ser	Cys	Glu	Pro
				135					140
Val	Thr	Ala	Ala	Glu	Leu	Asp	Ala	Lys	Glu
				145					150
Tyr	Arg	Met	Arg	Trp	Leu	Val	Arg	Thr	Ala
				155					160
His	Ala	Ala	Leu	Gly	Arg	Met	Met	Leu	Pro
				165					170

Lys	Leu	Met	Ala	Asp	Pro	Glu	Arg	Gly	Leu	
				175						180
Thr	Glu	Arg	Glu	Val	Glu	Val	Leu	Lys	Trp	
				185						190
Ala	Ala	Asp	Gly	Lys	Thr	Ser	Gly	Glu	Ile	
				195						200
Ser	Lys	Ile	Leu	Ala	Ile	Ser	Val	Asp	Thr	
				205						210
Val	Asn	Phe	His	Val	Lys	Asn	Ala	Ile	Leu	
				215						220
Lys	Leu	Arg	Thr	Ala	Asn	Lys	Thr	Ala	Ala	
				225						230
Val	Val	Arg	Ala	Ala	Met	Leu	Gly	Leu	Leu	
				235						240

Ser

<210> 29
 <211> 22
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 29

ccgcgacgac gacggggaaa tc 22

<210> 30
 <211> 23
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 30

togatccagc acgcgacgac cat 23

<210> 31
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 31

ataagcgccg cgcaactgga ttcc 24

<210> 32
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 32

caggatcgcc gtattgcggt gagc 24

<210> 33
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 33

tcgcgggccg attgaacgaa ctgc 24

<210> 34
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 34

gagcgacgcg gccaccgtga gcac 24

<210> 35
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 35

cggcttcgaa tattgctgct atgg 24

<210> 36
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 36

gagaaaacgg ctcatcagcg agtg 24

<210> 37
 <211> 23
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 37

agcgaccggc ccgtgacctg gag 23

<210> 38
 <211> 23

<212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 38

cggcctgtat cttgttcgtg gac 23

<210> 39
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 39

agaçgctcgtc tcgctgcact atcc 24

<210> 40
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 40

acccacgtga ggcacatctg ttcg 24

<210> 41
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 41

ggcgttcgac agatgaaaca cgac 24

<210> 42
 <211> 24
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer
 <400> 42

gctcatctgg cacgacgacc tcta 24

<210> 43
 <211> 22
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> designed primer

<400> 43

cgcggtgccgt ggccgctgtc ca

22

<210> 44

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> designed primer

<400> 44

ccgcgctccg ggtccgcat cag

23